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<110> Ebner et al.

<120> POLYNUCLEOTIDES ENCODING INTERLEUKIN-20

<130> PF399

<140> US 09/115,832
<141> 1998-07-15

<150> US 60/052,870
<151> 1997-07-16

<150> US 60/055,952
<151> 1997-08-18

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<151> 1997-09-26

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cac aac ctg ctg ttt ctt ctt acc att tcc atc ttc ctg ggg ctg ggc   104
His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe Leu Gly Leu Gly
    -15   -10   -5   -1

cag ccc agg agc ccc aaa agc aag agg aag ggg caa ggg cgg cct ggg   152
Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly Arg Pro Gly
1   5   10   15

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ccc ctg gcc cct ggc cct cac cag gtg cca ctg gac ctg gtg tca cgg      200
Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg
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atg aaa ccg tat gcc cgc atg gag gag tat gag agg aac atc gag gag      248
Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Ile Glu Glu
        35              40                  45

atg gtg gcc cag ctg agg aac agc tca gag ctg gcc cag aga aag tgt      296
Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys
    50              55                  60

gag gtc aac ttg cag ctg tgg atg tcc aac aag agg agc ctg tct ccc      344
Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro
65              70                  75                  80

tgg ggc tac agc atc aac cac gac ccc agc cgt atc ccc gtg gac ctg      392
Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu
                85                  90                  95

ccg gag gca cgg tgc ctg tgt ctg ggc tgt gtg aac ccc ttc acc atg      440
Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met
            100                 105                 110

cag gag gac cgc agc atg gtg agc gtg ccg gtg ttc agc cag gtt cct      488
Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro
        115                 120                 125

gtg cgc cgc cgc ctc tgc ccg cca ccg ccc cgc aca ggg cct tgc cgc      536
Val Arg Arg Arg Leu Cys Pro Pro Pro Arg Thr Gly Pro Cys Arg
    130                 135                 140

cag cgc gca gtc atg gag acc atc gct gtg ggc tgc acc tgc atc ttc      584
Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
145                 150                 155                 160

tgaattacct ggcccagaag ccaggccagc agcccgagac catcctcctt gcacctttgt     644

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a                                                                     705


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Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln
            -1   1               5                   10



Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
        15                  20                  25
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C¹
Cnt

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61

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Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
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```

```
Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala
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```

```
Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
            65              70              75
```

```
Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
            80              85              90
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```
Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn
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Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe
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```

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Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Arg Thr
125             130             135             140
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Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys
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Thr Cys Ile Phe
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Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
        35              40              45
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Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
    50              55              60
```

```
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65              70              75                      80

Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
            85              90                      95

Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
            100             105             110

Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
        115             120             125

Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
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Thr Cys Val Thr Pro Ile Val His His Val Ala
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cccaggagcc ccaaaagcaa gaggaagggg caagggcggc ctgggcccct ggncctggnc     180

ctcaccaggt gccactggac ctggtgtcac ggntgaaacc gtatcccgc atggaggagt      240

atgagaggaa catcgaggag atggtggccc agctgaggaa cagctcanag ctgggcccag     300

agaaagtttg angntcaact ttncaagctt ntgggtnttn caacaagnag gtagcctgtt     360

ttncntggng gttannagta tgaatncaag nancncangc gtnnntncng ttngnncttn     420

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<210>  7
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<223>  Contains a Bam HI restriction enzyme site and an efficient signal
       for initiation of translation in eukaryotic cells (Kozak, M., J.
       Mol. Biol. 196:947-950 (1987))

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Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
            35   40   45

Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
        50   55   60

Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala
65   70   75   80

Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
                85   90   95

Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
                100   105   110

Pro Val Asp Leu Pro Glu His Gly Ala Cys Val Trp Ala Val
                115   120   125